

1

Sequence listing

Sub B1

<110> Kaneka Corporation

5 <120> Process for producing coenzyme Q₁₀

<130> T549/QX-GT2

10 <150> JP P1999-237561

<151> 1999-08-24

<160> 2

<210> 1

15 <211> 1653

<212> DNA

<213> *Saioella complicata*

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aaatccatataccatg gcc tca cca gca ctg cgg ata cga agc atc agc 169

25 Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217

Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser

15

20

25

5

gca cct tca tta cga cta aga tgt acc ccg acg agc cgg cca tcg agt 265

Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser

30

35

40

10 tca tgg gct gct gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313

Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp

45

50

55

60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361

15 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met

65

70

75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409

Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro

20

80

85

90

tct ctc gac act gtc gct aaa tac tat gtt cag tct gag gga aag cat 457

Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His

95

100

105

25

att cgt ccg ctc atg gta ctg ctg atg gct cag gcg acg gag gtt gcg 505

Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala

110 115 120

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtg aac gag 553

5 Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu

125 130 135 140

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg 601

Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met

10 145 150 155

aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag 649

Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln

160 165 170

15

acg tcg aat atc ctc gcc tcg caa cgg cgg ttg gct gag atc acg gag 697

Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu

175 180 185

20 atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac gct tcc 745

Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser

190 195 200

gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag 793

25 Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys

205 210 215 220

atg gcg att ttg gct ggt gat ttc ttg ttg gga cgg gcg tct gtt gca 841
 Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala

225 230 235

5

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 Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val

240 245 250

10 att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt 937
 Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val

255 260 265

gat gat gcg att gag gct acg gcg acg cag gaa acg ttc gat tac tat 985
 15 Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr

270 275 280

ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc 1033
 Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
 20 285 290 295 300

aga gca agt gcg ctt ctg ggt ggt gct acg cct gag gtt gct gat gct 1081
 Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala

305 310 315

25

gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac 1129

Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp

320 325 330

gac atg ctc gac tac acc gtc tcc gct acc gac ctc ggt aag ccc gcc 1177

5 Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala

335 340 345

ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca 1225

Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala

10 350 355 360

tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct 1273

Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser

365 370 375 380

15

gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321

Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp

385 390 395

20 gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369

Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala

400 405 410

ttg gat gca att cgg acg ttc ccg gag agt ccg gca cgg aag gct ttg 1417

25 Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu

415 420 425

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467

Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg

430

435

440

5

cggtaaccggg ggatcctcta gagtcgacct gcaggcatgc aagcttggct gtttggcgg 1527

atgagagaag atttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

10 acagaatttg cctggcggca gtagcgcggt ggtcccacct gacccatgc cgaactcaga 1647

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<211> 440

<212> PRT

<213> Saioella complicata

20 <400> 2

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Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro

20 25 30

25 Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser

35 40 45

Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
 50 55 60
 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu
 65 70 75
 5 Met Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly
 80 85 90
 His Pro Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu
 95 100 105
 Gly Lys His Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala
 10 110 115 120
 Thr Glu Val Ala Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu
 125 130 135
 Val Pro Val Asn Glu Gly Leu Ala Pro Pro Glu Val Leu Asn Asp
 140 145 150
 15 Lys Asn Pro Asp Met Met Asn Met Arg Ser Gly Pro Leu Thr Lys
 155 160 165
 Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile Leu Ala Ser Gln
 170 175 180
 Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala Ala Ser Leu
 20 185 190 195
 Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg Asn Ala
 200 205 210
 Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu Ala
 215 220 225
 25 Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
 230 235 240

Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn
 245 250 255
 Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp
 260 265 270
 5 Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu
 275 280 285
 Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
 290 295 300
 Arg Ala Ser Ala Leu Leu Gly Ala Thr Pro Glu Val Ala Asp
 10 305 310 315
 Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile
 320 325 330
 Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly
 335 340 345
 15 Lys Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro
 350 355 360
 Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile
 365 370 375
 Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu
 20 380 385 390
 Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala
 395 400 405
 Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro
 410 415 420
 25 Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val
 425 430 435

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9

Leu Thr Arg Ser Arg

440